

**Amendments to the Specification:**

Please replace the paragraph beginning on page 13, line 10 with the following amended paragraph:

Figure 2 shows a High Performance Liquid Chromatography (HPLC) trace from the coupling reaction of a reactive tag of this invention with a synthetic peptide (HRDPYRFDPHKD - SEQ ID NO: 1);

Please replace the paragraph beginning on page 13, line 13 with the following amended paragraph:

Figure 3 shows a MALDI TOF MS spectrum of the peptide mixture shown in Figure 1 (HRDPYRFDPHKD - SEQ ID NO: 1);

Please replace the paragraph beginning on page 13, line 15 with the following amended paragraph:

Figure 4 shows a MALDI TOF MS spectrum from the labelling reaction of a synthetic peptide with a reactive MALDI matrix mass tag that comprises a linker (HSRGHRGHSHAHRG - SEQ ID NO: 9).

Please replace the paragraph beginning on page 13, line 18 with the following amended paragraph:

Figure 5a shows a schematic of the labelling protocol for beta-MSH  
(DEGPYKMEHFRWGSPPKD – SEQ ID NO: 5; DEGPYK – SEQ ID NO: 6;  
MEHFR – SEQ ID NO: 7; WGSPPKD – SEQ ID NO: 8).

Please replace the paragraph beginning on page 13, line 22 with the  
following amended paragraph:

Figure 6 shows spectra MALDI TOF for the unlabelled and labelled  
digests of beta-MSH (DEGPYK – SEQ ID NO: 6; MEHFR – SEQ ID NO: 7;  
WGSPPKD – SEQ ID NO: 8);

Please replace the paragraph beginning on page 14, line 4 with the  
following amended paragraph:

Figure 10 shows the results of a search for unmodified BSA peptides in the  
SWISSPROT database using the MS-Fit database search program (KYL YEIARR  
– SEQ ID NO: 10; KLVNELTEFAKT – SEQ ID NO: 11, RFKDLGEEHFKG –  
SEQ ID NO 12; RHPEYAVSVLLRL – SEQ ID NO: 13; KHLVDEPQNLIKQ –  
SEQ ID NO: 14; RRHPEYAVSVLLRL – SEQ ID NO: 15; KLGEYGFQNALIVRY  
– SEQ ID NO: 16; KDAFGLSFLYEYSRR – SEQ ID NO: 17;  
RKVPQVSTPTLVEVSRS – SEQ ID NO: 18; RMPCTEDYLSLILNRL – SEQ ID  
NO: 19; RRPCFSALTPDETYVPA – SEQ ID NO: 20; RHPYFYAPELLYYANKY  
– SEQ ID NO: 21; RRHPYFYAPELLYYANKY – SEQ ID NO: 22;  
RMPCTEDYLSLILNRLCVLHEKT – SEQ ID NO: 23;  
KHKPKATEEQ LKTVMENFVAFVDKCCAADDKE – SEQ ID NO: 24);

Please replace the paragraph beginning on page 14, line 10 with the following amended paragraph:

Figure 12 shows the results of a search for modified BSA peptides in the SWISSPROT database using the MS-Fit database search program (KVASLRE – SEQ ID NO: 25; KIETMRE – SEQ ID NO: 26; RCASIQKF – SEQ ID NO: 27; KAWSVARL – SEQ ID NO: 28; KSEIAHRF – SEQ ID NO: 29; RDTHKS – SEQ ID NO: 30; KYLYEIARR – SEQ ID NO: 31; RCASIQKF – SEQ ID NO: 32; KKFWGKY – SEQ ID NO: 33; KCCTESLVNRR – SEQ ID NO: 34; RHPEYAVSVLLRL – SEQ ID NO: 35; RALKAWSVARL – SEQ ID NO: 36; RRHPEYAVSVLLRL – SEQ ID NO: 37; KLGEYGFQNALIVRY – SEQ ID NO: 38; KVPQVSTPTLVEVSRS – SE SEQ ID NO: 39; KDAFLGSFLYEYSRR – SEQ ID NO: 40; RKVPQVSTPTLVEVSRS – SEQ ID NO: 41);

Please replace the paragraph beginning on page 14, line 16 with the following amended paragraph:

Figure 14 shows the results of a search for unmodified GAPDH peptides in the SWISSPROT database using the MS-Fit database search program (KAITIFQERD – SEQ ID NO: 42; RVPTPNVSVVDLTCRL – SEQ ID NO: 43; KAITIFQERDPANIKW – SEQ ID NO: 44; KLISWYDNEFGYSNRV – SEQ ID NO: 45; KVIHDHGIVEGLMTTVHAITATQKT – SEQ ID NO: 46; KVDVVAINDPFIDLHYMVYMFQYDSTHGKF – SEQ ID NO: 47; KWGDAGA EYVVESTGVFTTMEKAG AHLKGGAKRV – SEQ ID NO: 48);

Please replace the paragraph beginning on page 14, line 22 with the following amended paragraph:

Figure 16 shows the results of a search for modified GAPDH peptides in the SWISSPROT database using the MS-Fit database search program

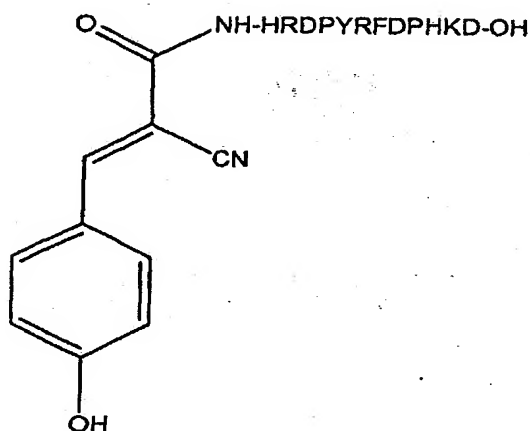
KGGAKRV – SEQ ID NO: 49; KLTGMAFRV – SEQ ID NO: 50; KVGVNFGFRI – SEQ ID NO: 51; KAGAHKLG – SEQ ID NO: 52; KAITIFQERD – SEQ ID NO: 53; KTVDGPSGKLWRD – SEQ ID NO: 54; RVPTPNVSVVDLTCRL – SEQ ID NO: 55; KYDDIKKVVVKQ – SEQ ID NO: 56; RDGRGAAQNIIPASTGAAKA – SEQ ID NO: 57; KLISWYDNEFGYSNRV – SEQ ID NO: 58);

Please replace the paragraph beginning on page 38, line 29 and ending on page 39, line 2 with the following amended paragraph:

The peptide sequence, HRDPYRFDPHKD (SEQ ID NO: 1), was synthesized on a Wang type resin using standard Fmoc/tBu synthesis procedures (see for example Fields G.B. & Noble R.L., Int J. Pept Protein Res 35(3): 161-214, "Solid phase peptide synthesis utilizing 9-flourenylmethoxycarbonyl amino acids." 1990). The resin-bound peptide yields a free acid moiety after cleavage.

Please replace the paragraph beginning on page 40, line 9 with the following amended paragraph:

NH-HRDPYRFDPHKD-COOH (SEQ ID NO: 1)



Molecular weight: 1753.87 g/mol (average) / 1752.78 g/mol (monoisotopic)

Mono-isotopic composition: C<sub>80</sub>H<sub>104</sub>N<sub>24</sub>O<sub>22</sub>

Please replace the paragraph beginning on page 41, line 10 with the following amended paragraph:

The following peptide sequences were synthesised on a Wang type resin using standard Fmoc/tBu synthesis procedures:

HSRGARGHSHAHRG (SEQ ID NO: 2) (highly basic) M:1522.62

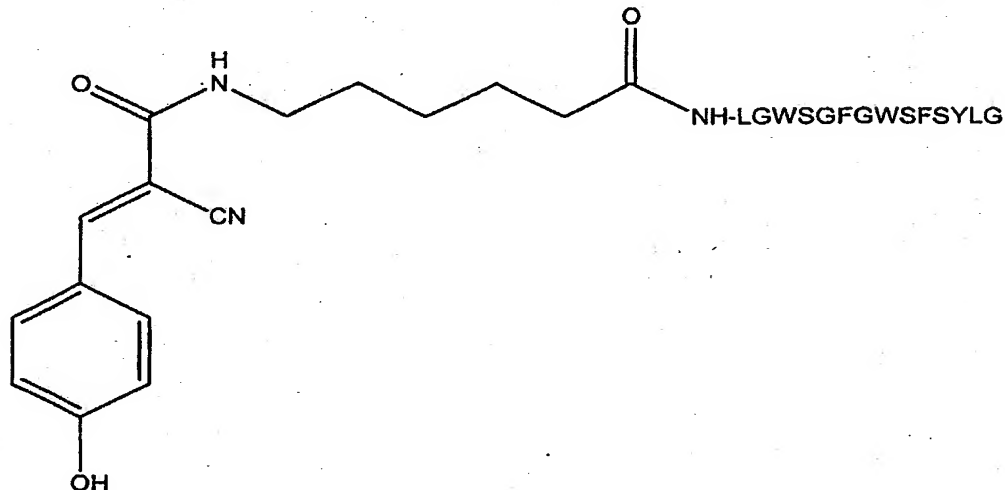
YDSGEGDESDAYEG (SEQ ID NO: 3) (highly acidic) M:1493.38

LGWSGFGWSFSYLG (SEQ ID NO: 4) (highly hydrophobic) M:1563.75

(bound to a trityl type resin to yield a free acid after cleavage)

Please replace the paragraph beginning on page 45, line 1 with the following amended paragraph:

NH-LGWSGFGWSFSYLG-COOH (SEQ ID NO: 4)



Molecular weight: 1848.06 g/mol (average) / 1846.84 g/mol (mono-isotopic)  
Mono-isotopic composition: C<sub>94</sub>H<sub>114</sub>N<sub>18</sub>O<sub>22</sub>.

Please replace the paragraph beginning on page 45, line 10 with the following amended paragraph:

The peptides were analysed by HPLC. The first peptide, HSRGARGHSHAHRG (SEQ ID NO: 2), was isolated pure as the reaction with the tag containing the linker went to completion. The labelled peptide was combined with unlabelled peptide to give a 50/50 mixture at a concentration of 1µmol/µl of each peptide. Analysis of the mixture by electrospray ionization mass spectrometry does not show any improvement in the sensitivity of detection of the labelled peptide compared to the unlabelled peptide. However, 0.5 µl of

the mixture on a metal target analysed by MALDI TOF MS shows that the labelled peptide is detected with greater sensitivity than the unlabelled peptide. This indicates that the linker functionality does not reduce the effectiveness of the tag and can be used to improve the yield of the labelling reaction.

Please replace the Table 2 beginning on page 47, line 9 with the following amended table:

m/z		Fragment Positions	Cleavage	Composition	
Isotopic Mass (Daltons)	Average Mass (Daltons)	Start	Finish	No. of reactive groups	Sequence
708.3204	708.7507	1	6	2	DEGPYK (SEQ ID NO: 6)
719.3299	719.8458	7	11	2	MEHFR (SEQ ID NO: 7)
786.3786	786.8682	12	18	2	WGSPPKD (SEQ ID NO: 8)

Please replace the Table 3 on page 47 with the following amended table:

m/z	Fragment Positions	Cleavage	Composition	
Isotopic Mass (Daltons)	Start	Finish	No. of tagged reactive groups	Sequence
992.435	1	6	1	DEGPYK +1 tag (SEQ ID NO: 6)
1276.535	1	6	2	DEGPYK +2 tags (SEQ ID NO: 6)
1003.445	7	11	1	MEHFR + 1 tag (SEQ ID NO: 7)
1287.560	7	11	2	MEHFR+ 2 tags (SEQ ID NO: 7)
1354.609	12	18	2	WGSPPKD + 2 tags (SEQ ID NO: 8)